



SEQUENCE LISTING

<110> Alitai, Kari
Joukov, Vladimir

<120> VASCULAR ENDOTHELIAL GROWTH FACTOR C (VEGF-C) PROTEIN
AND GENE, MUTANTS THEREOF, AND USES THEREOF

<130> 28967/34140A

<140> US 09/534,376

<141> 2000-03-24

<150> 09/355,700

<151> 1999-11-05

<150> PCT/US98/01973

<151> 1998-02-02

<150> 08/795,430

<151> 1997-02-05

<150> PCT/FI96/00427

<151> 1996-08-01

<150> 08/671,573

<151> 1996-06-28

<150> 08/601,132

<151> 1996-02-14

<150> 08/585,895

<151> 1996-01-12

<150> 08/510,133

<151> 1996-08-01

<150> 08/340,011

<151> 1994-11-14

<160> 59

<170> PatentIn Ver. 2.0

<210> 1

<211> 4416

<212> DNA

<213> Homo sapiens

<220>

<223> Human Flt4 cDNA (short form)

<220>

<223> At position 4243, n=A,T,G or C

<400> 1

ccacgcgcag cggccggaga tgcagcgggg cgccgcgctg tgccctgcgac tgtggctctg 60

cctggggactc ctggacggcc tggtagtggt ctactccatg acccccccca ccttgaacat 120

cacggaggag tcacacgtca tcgacacggg tgacagcctg tccatctcct gcagggggaca 180

gcaacccctc gagggggctt ggccaggagc tcaggagggc ccagccaccg gagacaagga 240
 cagcgaggac acgggggttg tgcgagactg cgagggcaca gacgcaggc cctactgaa 300
 ggtgttgctg ctgcacgagg tacatgccaa cgacacaggc agctacgtct gctactaaa 360
 gtacatcaag gcacgccttg agggcaccac ggccgccagc tctacgtgt tctgagaga 420
 ctttgagcag ccattcatca acaagcctga cagctcttg gtcaacagga aggacgccat 480
 gtgggtgcc tgtctggtgt ccatcccg cctcaatgtc acgtgcgtc cgaaaagctc 540
 ggtgctgttg ccagacgggc aggaggtggt gtgggatgac cggcggggca tctcgtgtc 600
 cagccactg ctgcacgatg cctgtacct gcagtgcgag accacctgg gagaccagga 660
 cttctttcc aacctctcc tgggtcacat cacaggcaac gagctctatg acatccagct 720
 gttgccagg aagtccttg agctgctggt aggggagaag ctggtcctga actgcaccgt 780
 gtgggtgag tttaactcag gtgtcacctt tgactgggac taccagggga agcaggcaga 840
 gcggggttaag tgggtgcccg agcgacgtc ccagcagacc cacacagaac tctccagcat 900
 cctgaccatc cacaacgtca gccagcacga cctgggctcg tatgtgtgca aggccaaaca 960
 cggcatccag cgatttcggg agagcacga ggtcattgtg catgaaaac ccttcacag 1020
 cgtcgagtgg ctcaaaggac ccatcctgga ggccacggca ggagacgagc tggtaagct 1080
 gcctgtgaag ctggcagcgt aaccccgcc cgagttccag tggtaaaagg atggaaaggc 1140
 actgtccgg cgccacagtc cacatgcct ggtgctcaag gaggtgacag aggcacgac 1200
 aggcacctac acctcgccc tgtggaactc cgtgctggc ctgaggcga acatcagcct 1260
 ggagctggtg gtgaatgtgc cccccagat acatgagaag gaggcctct ccccagcat 1320
 ctactcgtt cacagccgc aggcctcac ctgcacggc tacgggtgc cctgcctct 1380
 cagcatccag tggcactggc ggccctggac acctgcaag atgtttgcc agcgtagtct 1440
 ccggcggcg cagcagcaag acctcatgcc acagtgcct gactggaggg cggtgaccac 1500
 gcaggatgcc gtgaacccca tcgagagcct ggacacctgg accgagttt tggagggaaa 1560
 gaataagact gtgagcaagc tgggtgatca gaatgccaa gtgtctgca tgtacaagt 1620
 tgtggtctc aacaagggtg gccaggatga gcggctcct tacttctatg tgaccacat 1680
 ccccgacggc ttaccatcg aatccaagc atccgaggag ctactagagg gccagccgt 1740
 gctcctgagc tgccaagccg acagctaaa gtacgagcat ctgcgtggt accgctcaa 1800
 cctgtccag ctgcacgatg cgcacgggaa cccgttctg ctgactgca agaactgca 1860
 tctgttcgc acctctctg ccgcagcct ggaggaggtg gcacctggg cggccacgc 1920
 cagctcagc ctgagtatc cccgcgtgc gcccgagcag gagggcact atgtgtgca 1980
 agtgcaagac cgggcagcc atgacaagca ctgcacaag aagtacctgt cggtgaggc 2040
 cctggaagc cctgggtca cggagaactt gaccgacctc ctggtgaac ttagcactc 2100

getggagatg cagtgetttg tggcgggagc gaacgcgcgc agcatcgtgt ggtacaaaga 2160
 cgagagggtg ctggaggaaa agtctggagt cgacttggcg gactccaaac agaagctgag 2220
 catccagcgc gtgcgggagg aggatgcggg acgctatctg tgcagcgtgt gcaacgcgca 2280
 gggctgcgt : aactcctcgc ccagcgtggc cgtggaaggc tcgaggata agggcagcat 2340
 ggagatcgtg atccttgctg gtacggggct catcgtctgc ttctctcggg cctcctcct 2400
 cctcatcttc tgtaacatga ggaggccggc ccacgcagac atcaagacgg gctacctgtc 2460
 catcatcatg gaccccgggg aggtgcctct ggaggagcaa tgcgaatacc tgtctacga 2520
 tgccagccag tgggaattcc ccgagagcgc gctgcacctg gggagagtgc tcggctacgg 2580
 cgccttcggg aaggtgggtg aagcctcgc ttccggcctc cacaagggca gcagctgtga 2640
 caccgtggcc gtgaaaatgc tgaaagaggc cgcacggcc agcgagcacc gcgcgtgat 2700
 gtccgagctc aagatcctca ttcacatcgc caaccacctc aacgtggcca acctcctcgc 2760
 ggctgcacc aagccgcagg gccccctcat ggtgatcgtg gagttctgca agtacggcaa 2820
 cctctccaac ttctgcgcg ccaagcggga cgccttcagc cctgcgcgg agaagtctcc 2880
 cgagcagcgc ggacgccttc gcgccatggt ggagctcgc aggcctggatc ggaggcggcc 2940
 ggggagcagc gacagggctc tcttcgcgcg gttctcgaag accgaggcgc gagcgaggcg 3000
 ggcttctcca gaccaagaag ctgaggacct gtggctgagc ccgctgacca tggaagatct 3060
 tgtctgctac agcttcacag tggccagagg gatggagttc ctggcttccc gaaagtgcct 3120
 ccacagagac ctggctgtc ggaacattct gctgtcggaa agcgacgtgg tgaagatctg 3180
 tgaacttggc ctgccccggg acatctacaa agaccctgac tacgtccgca agggcagtc 3240
 ccgctgccc ctgaagtgga tggccccga aagcatcttc gacaagggtg acaccacgca 3300
 gagtgacgtg tggctccttg ggggtgcttct ctgggagatc ttctctctgg gggcctccc 3360
 gtaccctggg gtgcagatca atgaggagtt ctgccagcgc ctgagagacg gcacaaggat 3420
 gagggccccg gagctggcca ctcccgccat acgcgcctc atgctgaact gctggctcgg 3480
 agaccccaaag gcgagacctg cattctcgga gctgggtggag atcctggggg acctgctcca 3540
 gggcaggggc ctgcaagagg aagaggaggt ctgcatggcc ccgcgcagct ctgagagctc 3600
 agaagagggc agcttctcgc aggtgtccac catggcccta cacatcgccc aggcagacgc 3660
 tgaggacagc ccgccaagcc tgcagcgcca cagcctggcc gccaggtatt acaactgggt 3720
 gtccttctcc ggggtgcctg ccagaggggc tgagaccctg ggttcctcca ggatgaagac 3780
 atttgaggaa tccccatga cccaacgac ctacaaaggc tctgtggaca accagacaga 3840
 cagtgggatg gtgctggcct cggaggagtt tgagcagata gagagcaggc atagacaaga 3900
 aagcggcttc aggtagctga agcagagaga gagaaggcag catacgtcag cattttcttc 3960
 tctgcactta taagaaagat caaagacttt aagactttcg ctatttcttc tactgctatc 4020

tactacaaac ttcaaagagg aaccaggagg acaagaggag catgaaagtg gacaaggagt 4080
 gtgaccactg aagcaccaca gggaaggggt taggcctccg gatgactgcg ggcaggcctg 4140
 gataatatcc agcctccccc aagaagctgg tggagtagag tgttcctga ctctccaag 4200
 gaaagggaga cgccttttca tggctctgtg agtaacaggt gcnttcccag acactggcgt 4260
 tactgcttga ccaaagagcc ctcaagcggc ccttatgcca gcgtgacaga gggctcacct 4320
 cttgccttct aggtcacttc tcacacaatg tcccttcage acctgacct gtgcccgcga 4380
 gttattcctt ggtaatatga gtaatacatc aaagag 4415

<210> 2
 <211> 216
 <212> DNA
 <213> Homo sapiens

<220>
 <223> Human Flt4 cDNA (3' end-long form)

<400> 2
 caagaaagcg gcttcagctg taaaggacct ggccagaatg tggctgtgac cagggcacac 60
 cctgactccc aaggaggcg gcggcgccct gagcgggggg cccgaggagg ccagggtgttt 120
 tacaacagcg agtatgggga gctgtcggag ccaagcgagg aggaccactg ctccccgtct 180
 gccgcgctga ctttcttcac agacaacagc tactaa 215

<210> 3
 <211> 4273
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: pLTRpoly
 vector

<400> 3
 aagcttatcg atttcgaacc cgggggtacc gaattcctcg agtctagagg agcatgcctg 60
 caggctgacc gggctcgatc cctcgcgag ttgggtcage tgctgcctga ggctggacga 120
 cctcgcgag ttctaccggc agtgcaaacc cgtcggcatc caggaaacca gcagcggcta 180
 tccgcgcac catgcccccg aactgcagga gtggggaggc acgatggccg ctttgggtccc 240
 ggatctttgt gaaggaacct tacttctgtg gtgtgacata attggacaaa ctacctacag 300
 agatttaaag ctctaaggta aatataaaat ttttaagtgt ataattgtgt aaactactga 360
 ttctaattgt ttgtgtatct tagattccaa cctatggaac tgatgaatgg gagcagtggg 420
 ggaatgcctt taatgaggaa aacctgtttt gctcagaaga aatgccatct agtgatgatg 480
 aggtactgc tgactctcaa cattctactc ctccaaaaaa gaagagaaag gtagaagacc 540
 ccaaggactt tccttcagaa ttgctaagtt ttttgagtca tgctgtgttt agtaatagaa 600

ctcttgettg ctttgetatt tacaccacaa aggaaaaaagc tgcactgcta tacaagaaaa 660
 ttatggaaaa atattctgta acctttataa gtaggcataa cagttataat cataacatac 720
 tgttttttct tactccacac aggcatagag tgtctgctat taataactat gctcaaaaat 780
 tgtgtacctt tagcttttta atttgtaaag gggttaataa ggaatatttg atgtatagt 840
 ccttgactag agatcataat cagccatacc acatttgtag aggttttact tgctttaaaa 900
 aaactccac acctccccct gaacctgaaa cataaaatga atgcaattgt tgttgtaac 960
 ttgtttattg cagcttataa tggttacaaa taaagcaata gcatcacaaa ttccacaaat 1020
 aaagcatttt ttccactgca ttctagttgt ggtttgtcca aactcatcaa tgtatcttat 1080
 catgtctgga tetgcccgtc tccctatagt gagtcgtatt aatttcgata agccaggtta 1140
 acctgcatta atgaatcggc caacgcgcgg ggagaggcgg tttgcgtatt gggcgcctct 1200
 ccgttctctc gctcactgac tegetgcgct cggtcgttcg gctgcggcga gcggtatcag 1260
 ctactcaaa ggcggaata cggttatcca cagaatcagg ggataacgca ggaaagaaca 1320
 tgtgagcaaa aggcagcaa aaggccagga accgtaaaaa ggacgcgttg ctggcgtttt 1380
 tccataggct ccgccccct gacgagcatc acaaaaatcg acgctcaagt cagagggtggc 1440
 gaaacccgac aggactataa agataccagg cgtttcccc cggaaagctcc ctctgcgct 1500
 ctctgttcc gacctgcgc cttaccggat acctgtccgc cttctccct tcgggaagcg 1560
 tggcgttttc tcaatgctca cgtctaggt atctcagttc ggtgtaggtc gtctgcctca 1620
 agctgggctg tgtgcacgaa cccccgttc agcccgaccg ctgcgcctta tccggaact 1680
 atcgtcttga gtccaaccgc gtaagacacg acttatcgcc actggcagca gccactggta 1740
 acaggattag cagagcgagg tatgtaggcg gtgctacaga gttcttgaag tgggtggccta 1800
 actacggcta cactagaagg acagtatttg gtatctgcgc tctgctgaag ccagttacct 1860
 tcggaaaaag agttggtagc tottgatccg gcaaacaaac caccgctggt agcggtggtt 1920
 tttttgttg caagcagcag attacgcgc gaaaaaaagg atctcaagaa gatcctttga 1980
 tcttttctac ggggtctgac gctcagtga acgaaaactc acgttaaggg attttggtca 2040
 tgagattatc aaaaaggatc ttcacctaga tctttttaa ttaaaaatga agttttaaat 2100
 caatctaaag tatatatgag taaacttggt ctgacagtta ccaatgctta atcagtgagg 2160
 cacctatctc agcgatctgt ctatttcgtt catccatagt tgctgactc cccgtcgtgt 2220
 agataactac gatacgggag ggcttaccat ctggccccag tgctgcaatg ataccgcgag 2280
 acccagctc accggctcca gatattatcag caataaacca gccagccgga agggccgagc 2340
 gcagaagtgg tctgcaact ttatccgct ccattccagtc tattaattgt tgccgggaag 2400
 ctagagtaag tagttcgcca gttaatagtt tgcgcaacgt tgttgccatt gctacaggca 2460
 tctgggtgct acgctcgtcg tttggtatgg ctccatcag ctccgggttc caacgatcaa 2520

ggagagttac atgatcccc atgttggtgca aaaaagcggg tagctccttc ggctcctcga 2580
 tcgttggtcag aagtaagttg gccgcagtgt taccactcat ggttatggca gcaactgcata 2640
 attctcttac tgcacatgcca tccgtaagat gcttttctgt gactggtgag tactcaacca 2700
 agtcattctg agaatagtgt atgcggcgac cgagttgctc ttgcgcggcg tcaatacggg 2760
 ataataccgc gccacatagc agaactttaa aagtgtctat cattggaaaa cgttcttcgg 2820
 ggcgaaaact ctcaaggatc ttaccgctgt tgagatccag ttcatgtaa cccactcgtg 2880
 caccacaactg atcttcagca tcttttactt tcaccagcgt ttctgggtga gcaaaaacag 2940
 gaaggcaaaa tgcgcgaaaa aagggaataa ggcgcacacg gaaatgttga atactcatac 3000
 tcttcctttt tcaatattat tgaagcattt atcaggggta ttgtctcatg agcggatata 3060
 tatttgaatg tatttagaaa aataaataa taggggttcc gcgcacattt ccccgaaaag 3120
 tgccacctga cgtctaagaa accattatta tcatgacatt aacctataaa aataggcgta 3180
 tcacgaggcc ctttcgtctc gcgcgtttcg gtgatgacgg tgaaaacctc tgacacatgc 3240
 agtccccga gacggtcaca gcttgctgtg aagcggatgc cgggagcaga caagcccgtc 3300
 agggcgctgc agcgggtgtt ggcgggtgtc ggggctggct taactatgcg gcatcagagc 3360
 agattgtact gagagtgcac catatggaca tattgtcgtt agaacgcggc tacaattaat 3420
 acataacctt atgtatcata cacatacgat ttaggtgaca ctatagaact cgagcagagc 3480
 ttccaaattg agagagaggg ttaatcagag acagaaactg tttgagtcaa ctcaaggatg 3540
 gtttgagggg ctgtttaaca gatccccctg gtttaccacc ttgatatacta ccattatggg 3600
 accctcatt gtactcctaa tgattttgct cttcggacct tgcattctta atcgattagt 3660
 ccaatttgtt aaagacagga taccagtggc ccaggctcta gttttgactc aacaatatca 3720
 ccagctgaag cctatagagt acgagccata gataaaataa aagattttat ttagtctcca 3780
 gaaaaagggg ggaatgaaag accccacctg taggtttggc aagctagctt aagtaacgcc 3840
 attttgcaag gcatggaaaa atacataact gagaatagag aagttcagat caaggtcagg 3900
 aacagatgga acagctgaat atggggccaa caggatatct gtggttaagca gttcctgccc 3960
 cggctcaggg ccaagaacag atggaacagc tgaatatggg ccaaacagga tatctgtggt 4020
 aagcagttcc tgccccggct caggggccaa aacagatggt cccagatgc ggtccagccc 4080
 tcagcagttt ctagagaacc atcagatggt tccagggtgc cccaaggacc tgaaatgacc 4140
 ctgtgcctta tttgaactaa ccaatcagtt cgtttctcgc ttctgttcgc gcgcttctgc 4200
 tccccagct caataaaaaga gccacacaacc cctcactcgg ggcgccagtc ctccgattga 4260
 ctgagtcgcc cgg 4273

<210> 4
 <211> 40

<212> PPT
<213> Homo sapiens

<220>
<223> Flt4 C-terminal peptide

<400> 4
Pro Met Thr Pro Thr Thr Tyr Lys Gly Ser Val Asp Asn Gln Thr Asp
1 5 10 15
Ser Gly Met Val Leu Ala Ser Glu Glu Phe Glu Gln Ile Glu Ser Arg
20 25 30
His Arg Gln Glu Ser Gly Phe Arg
35 40

<210> 5
<211> 18
<212> PPT
<213> Homo sapiens

<220>
<223> At position 1, Xaa = Unknown

<220>
<223> N-terminal sequence from VEGF-C purified from PC-3
conditioned medium

<400> 5
Xaa Glu Glu Thr Ile Lys Phe Ala Ala Ala His Tyr Asn Thr Glu Ile
1 5 10 15
Leu Lys

<210> 6
<211> 219
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: vector and
human VEGF-C cDNA

<400> 6
tcactatagg gagaccaag cttggtaccg agctcggatc cactagtaac ggccgccagt 60
gtgggtggaat tcgacgaact catgactgta ctctaccag aatattggaa aatgtacaag 120
tgtcagctaa ggcaaggagg ctggcaacat aacagagaac aggccaacct caactcaagg 180
acagaagaga ctataaaatt cgctgcagca cactacaac 219

<210> 7
<211> 1997
<212> DNA
<213> Homo sapiens

<220>
<221> CDS

<222> (352)...(1608)

<220>

<223> prepro VEGF C cDNA

<400> 7

```
ccccccccgc ctctccaaaa agctacaccg acgcggaccg cggcggcgctc ctccctcgcc 60
ctcgcttcac ctgcggggct ccgaatgcgg ggagctcgga tgtccggttt cctgtgaggg 120
ttttacctga caccgcgcgc ctttccccgg cactggctgg gagggcgccc tgcaaagttg 180
ggaacgcgga gccccggacc cgtcccgcc gcctccggct cggccagggg gggtcgccc 240
gaggagcccc ggggagaggg accaggaggg gcccgcgccc tcgcaggggc gcccgcccc 300
ccacccctgc ccccgccagc ggaccggctc cccacccccg gtccttcac c atg cac 357
                                         Met His
                                         1

ttg ctg ggc ttc ttc tct gtg gcg tgt tct ctg ctc gcc gct gcg ctg 405
Leu Leu Gly Phe Phe Ser Val Ala Cys Ser Leu Leu Ala Ala Leu
                    5                      10                      15

ctc ccg ggt cct cgc gag gcg ccc gcc gcc gcc gcc gcc ttc gag tcc 453
Leu Pro Gly Pro Arg Glu Ala Pro Ala Ala Ala Ala Ala Phe Glu Ser
                20                      25                      30

gga ctc gac ctc tcg gac gcg gag ccc gac gcg ggc gag gcc acg gct 501
Gly Leu Asp Leu Ser Asp Ala Glu Pro Asp Ala Gly Glu Ala Thr Ala
                35                      40                      45

tat gca agc aaa gat ctg gag gag cag tta cgg tct gtg tcc agt gta 549
Tyr Ala Ser Lys Asp Leu Glu Glu Gln Leu Arg Ser Val Ser Ser Val
                    55                      60                      65

gat gaa ctc atg act gta ctc tac cca gaa tat tgg aaa atg tac aag 597
Asp Glu Leu Met Thr Val Leu Tyr Pro Glu Tyr Trp Lys Met Tyr Lys
                    70                      75                      80

tgt cag cta agg aaa gga ggc tgg caa cat aac aga gaa cag gcc aac 645
Cys Gln Leu Arg Lys Gly Gly Trp Gln His Asn Arg Glu Gln Ala Asn
                    85                      90                      95

ctc aac tca agg aca gaa gag act ata aaa ttt gct gca gca cat tat 693
Leu Asn Ser Arg Thr Glu Glu Thr Ile Lys Phe Ala Ala Ala His Tyr
                    100                      105                      110

aat aca gag atc ttg aaa agt att gat aat gag tgg aga aag act caa 741
Asn Thr Glu Ile Leu Lys Ser Ile Asp Asn Glu Trp Arg Lys Thr Gln
                    115                      120                      125                      130

tgc atg cca cgg gag gtg tgt ata gat gtg ggg aag gag ttt gga gtc 789
Cys Met Pro Arg Glu Val Cys Ile Asp Val Gly Lys Glu Phe Gly Val
                    135                      140                      145

gcg aca aac acc ttc ttt aaa cct cca tgt gtg tcc gtc tac aga tgt 837
Ala Thr Asn Thr Phe Phe Lys Pro Pro Cys Val Ser Val Tyr Arg Cys
                    150                      155                      160

ggg ggt tgc tgc aat agt gag ggg ctg cag tgc atg aac acc agc acg 885
Gly Gly Cys Cys Asn Ser Glu Gly Leu Gln Cys Met Asn Thr Ser Thr
                    165                      170                      175
```


agc tac ctc agc aag acg tta ttt gaa att aca gtg cct ctc tct caa 933
 Ser Tyr Leu Ser Lys Thr Leu Phe Glu Ile Thr Val Pro Leu Ser Gln
 180 185 190

ggc ccc aaa cca gta aca atc agt ttt gcc aat cac act tcc tgc cga 981
 Gly Pro Lys Pro Val Thr Ile Ser Phe Ala Asn His Thr Ser Cys Arg
 195 200 205 210

tgc atg tct aaa ctg gat gtt tac aga caa gtt cat tcc att att aga 1029
 Cys Met Ser Lys Leu Asp Val Tyr Arg Gln Val His Ser Ile Ile Arg
 215 220 225

cgt tcc ctg cca gca aca cta cca cag tgt cag gca gcg aac aag acc 1077
 Arg Ser Leu Pro Ala Thr Leu Pro Gln Cys Gln Ala Ala Asn Lys Thr
 230 235 240

tgc ccc acc aat tac atg tgg aat aat cac atc tgc aga tgc ctg gct 1125
 Cys Pro Thr Asn Tyr Met Trp Asn Asn His Ile Cys Arg Cys Leu Ala
 245 250 255

cag gaa gat ttt atg ttt tcc tgc gat gct gga gat gac tca aca gat 1173
 Gln Glu Asp Phe Met Phe Ser Ser Asp Ala Gly Asp Asp Ser Thr Asp
 260 265 270

gga ttc cat gac atc tgt gga cca aac aag gag ctg gat gaa gag acc 1221
 Gly Phe His Asp Ile Cys Gly Pro Asn Lys Glu Leu Asp Glu Glu Thr
 275 280 285 290

tgt cag tgt gtc tgc aga gcg ggg ctt cgg cct gcc agc tgt gga ccc 1269
 Cys Gln Cys Val Cys Arg Ala Gly Leu Arg Pro Ala Ser Cys Gly Pro
 295 300 305

cac aaa gaa cta gac aga aac tca tgc cag tgt gtc tgt aaa aac aaa 1317
 His Lys Glu Leu Asp Arg Asn Ser Cys Gln Cys Val Cys Lys Asn Lys
 310 315 320

ctc ttc ccc agc caa tgt ggg gcc aac cga gaa ttt gat gaa aac aca 1365
 Leu Phe Pro Ser Gln Cys Gly Ala Asn Arg Glu Phe Asp Glu Asn Thr
 325 330 335

tgc cag tgt gta tgt aaa aga acc tgc ccc aga aat caa ccc cta aat 1413
 Cys Gln Cys Val Cys Lys Arg Thr Cys Pro Arg Asn Gln Pro Leu Asn
 340 345 350

cct gga aaa tgt gcc tgt gaa tgt aca gaa agt cca cag aaa tgc ttg 1461
 Pro Gly Lys Cys Ala Cys Glu Cys Thr Glu Ser Pro Gln Lys Cys Leu
 355 360 365 370

tta aaa gga aag aag ttc cac cac caa aca tgc agc tgt tac aga cgg 1509
 Leu Lys Gly Lys Lys Phe His His Gln Thr Cys Ser Cys Tyr Arg Arg
 375 380 385

cca tgt acg aac cgc cag aag gct tgt gag cca gga ttt tca tat agt 1557
 Pro Cys Thr Asn Arg Gln Lys Ala Cys Glu Pro Gly Phe Ser Tyr Ser
 390 395 400

gaa gaa gtg tgt cgt tgt gtc cct tca tat tgg aaa aga cca caa atg 1605
 Glu Glu Val Cys Arg Cys Val Pro Ser Tyr Trp Lys Arg Pro Gln Met
 405 410 415

agc taagattgta ctgttttcca gttcatcgat tttctattat ggaaaactgt 1658
 Ser

gttgccacag tagaactgtc tgtgaacaga gagacccttg tgggtccatg ctaacaaaga 1718
 caaaagtctg tctttcttga accatgtgga taactttaca gaaatggact ggagctcacc 1778
 tgcaaaaggc ctcttgtaaa gactgggttt ctgccaatga ccaaacagcc aagattttcc 1838
 tcttggtgatt tctttaaaag aatgactata taattttatt ccactaaaaa tattgtttct 1898
 gcattcattt ttatagcaac aacaattggt aaaactcact gtgatcaata tttttatata 1958
 atgcaaaata tgtttaaaat aaaatgaaaa ttgtattat 1997

<210> 8
 <211> 419
 <212> PRT
 <213> Homo sapiens

<400> 8
 Met His Leu Leu Gly Phe Phe Ser Val Ala Cys Ser Leu Leu Ala Ala
 1 5 10 15
 Ala Leu Leu Pro Gly Pro Arg Glu Ala Pro Ala Ala Ala Ala Ala Phe
 20 25 30
 Glu Ser Gly Leu Asp Leu Ser Asp Ala Glu Pro Asp Ala Gly Glu Ala
 35 40 45
 Thr Ala Tyr Ala Ser Lys Asp Leu Glu Glu Gln Leu Arg Ser Val Ser
 50 55 60
 Ser Val Asp Glu Leu Met Thr Val Leu Tyr Pro Glu Tyr Trp Lys Met
 65 70 75 80
 Tyr Lys Cys Gln Leu Arg Lys Gly Gly Trp Gln His Asn Arg Glu Gln
 85 90 95
 Ala Asn Leu Asn Ser Arg Thr Glu Glu Thr Ile Lys Phe Ala Ala Ala
 100 105 110
 His Tyr Asn Thr Glu Ile Leu Lys Ser Ile Asp Asn Glu Trp Arg Lys
 115 120 125
 Thr Gln Cys Met Pro Arg Glu Val Cys Ile Asp Val Gly Lys Glu Phe
 130 135 140
 Gly Val Ala Thr Asn Thr Phe Phe Lys Pro Pro Cys Val Ser Val Tyr
 145 150 155 160
 Arg Cys Gly Gly Cys Cys Asn Ser Glu Gly Leu Gln Cys Met Asn Thr
 165 170 175
 Ser Thr Ser Tyr Leu Ser Lys Thr Leu Phe Glu Ile Thr Val Pro Leu
 180 185 190
 Ser Gln Gly Pro Lys Pro Val Thr Ile Ser Phe Ala Asn His Thr Ser
 195 200 205
 Cys Arg Cys Met Ser Lys Leu Asp Val Tyr Arg Gln Val His Ser Ile
 210 215 220

Ile Arg Arg Ser Leu Pro Ala Thr Leu Pro Gln Cys Gln Ala Ala Asn
 225 230 235 240
 Lys Thr Cys Pro Thr Asn Tyr Met Trp Asn Asn His Ile Cys Arg Cys
 245 250 255
 Leu Ala Gln Glu Asp Phe Met Phe Ser Ser Asp Ala Gly Asp Asp Ser
 260 265 270
 Thr Asp Gly Phe His Asp Ile Cys Gly Pro Asn Lys Glu Leu Asp Glu
 275 280 285
 Glu Thr Cys Gln Cys Val Cys Arg Ala Gly Leu Arg Pro Ala Ser Cys
 290 295 300
 Gly Pro His Lys Glu Leu Asp Arg Asn Ser Cys Gln Cys Val Cys Lys
 305 310 315 320
 Asn Lys Leu Phe Pro Ser Gln Cys Gly Ala Asn Arg Glu Phe Asp Glu
 325 330 335
 Asn Thr Cys Gln Cys Val Cys Lys Arg Thr Cys Pro Arg Asn Gln Pro
 340 345 350
 Leu Asn Pro Gly Lys Cys Ala Cys Glu Cys Thr Glu Ser Pro Gln Lys
 355 360 365
 Cys Leu Leu Lys Gly Lys Lys Phe His His Gln Thr Cys Ser Cys Tyr
 370 375 380
 Arg Arg Pro Cys Thr Asn Arg Gln Lys Ala Cys Glu Pro Gly Phe Ser
 385 390 395 400
 Tyr Ser Glu Glu Val Cys Arg Cys Val Pro Ser Tyr Trp Lys Arg Pro
 405 410 415
 Gln Met Ser

<210> 9
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: peptide

<220>
 <223> VEGF-C peptide "PAM126"

<400> 9
 Glu Glu Thr Ile Lys Phe Ala Ala Ala His Tyr Asn Thr Glu Ile Leu
 1 5 10 15

Lys

<210> 10
 <211> 1836
 <212> DNA
 <213> Murine

<220>

<221> CDS

<222> (168) .. (1412)

<220>

<221> cDNA encoding murine VEGF C precursor

<400> 10

gcgggcgcgt cgacgcaaaa gttgcgagcc gccgagtcgc gggagacgct cgcccagggg 60

gggtcccggg aggaaccac gggacagga ccaggagagg acctcagcct cagccccag 120

cctgcgcag ccaacggacc ggctccctg ctcccggtcc atccacc atg cac ttg 176
Met His Leu
1

ctg tgc ttc ttg tct ctg gcg tgt tcc ctg ctc gcc gct gcg ctg atc 224
Leu Cys Phe Leu Ser Leu Ala Cys Ser Leu Leu Ala Ala Leu Ile
5 10 15

ccc agt ccg cgc gag gcg ccc gcc acc gtc gcc gcc ttc gag tcg gga 272
Pro Ser Pro Arg Glu Ala Pro Ala Thr Val Ala Ala Phe Glu Ser Gly
20 25 30 35

ctg ggc ttc tcg gaa gcg gag ccc gac ggg ggc gag gtc aag gct ttt 320
Leu Gly Phe Ser Glu Ala Glu Pro Asp Gly Gly Glu Val Lys Ala Phe
40 45 50

gaa ggc aaa gac ctg gag gag cag ttg cgg tct gtg tcc agc gta gat 368
Glu Gly Lys Asp Leu Glu Glu Gln Leu Arg Ser Val Ser Ser Val Asp
55 60 65

gag ctg atg tct gtc ctg tac cca gac tac tgg aaa atg tac aag tgc 416
Glu Leu Met Ser Val Leu Tyr Pro Asp Tyr Trp Lys Met Tyr Lys Cys
70 75 80

cag ctg cgg aaa ggc ggc tgg cag cag ccc acc ctc aat acc agg aca 464
Gln Leu Arg Lys Gly Gly Trp Gln Gln Pro Thr Leu Asn Thr Arg Thr
85 90 95

ggg gac agt gta aaa ttt gct gct gca cat tat aac aca gag atc ctg 512
Gly Asp Ser Val Lys Phe Ala Ala Ala His Tyr Asn Thr Glu Ile Leu
100 105 110 115

aaa agt att gat aat gag tgg aga aag act caa tgc atg cca cgt gag 560
Lys Ser Ile Asp Asn Glu Trp Arg Lys Thr Gln Cys Met Pro Arg Glu
120 125 130

gtg tgt ata gat gtg ggg aag gag ttt gga gca gcc aca aac acc ttc 608
Val Cys Ile Asp Val Gly Lys Glu Phe Gly Ala Ala Thr Asn Thr Phe
135 140 145

ttt aaa cct cca tgt gtg tcc gtc tac aga tgt ggg ggt tgc tgc aac 656
Phe Lys Pro Pro Cys Val Ser Val Tyr Arg Cys Gly Gly Cys Cys Asn
150 155 160

agc gag ggg ctg cag tgc atg aac acc agc aca ggt tac ctc agc aag 704
Ser Glu Gly Leu Gln Cys Met Asn Thr Ser Thr Gly Tyr Leu Ser Lys
165 170 175

acg ttg ttt gaa att aca gtg cct ctc tca caa ggc ccc aaa cca gtc 752
Thr Leu Phe Glu Ile Thr Val Pro Leu Ser Gln Gly Pro Lys Pro Val
180 185 190 195

aca atc agt ttt gcc aat cac act tcc tgc cgg tgc atg tct aaa ctg 800
 Thr Ile Ser Phe Ala Asn His Thr Ser Cys Arg Cys Met Ser Lys Leu
 200 205 210

gat gtt tac aga caa gtt cat tca att att aga cgt tct ctg cca gca 848
 Asp Val Tyr Arg Gln Val His Ser Ile Ile Arg Arg Ser Leu Pro Ala
 215 220 225

aca tta cca cag tgt cag gca gct aac aag aca tgt cca aca aac tat 896
 Thr Leu Pro Gln Cys Gln Ala Ala Asn Lys Thr Cys Pro Thr Asn Tyr
 230 235 240

gtg tgg aat aac tac atg tgc cga tgc ctg gct cag cag gat ttt atc 944
 Val Trp Asn Asn Tyr Met Cys Arg Cys Leu Ala Gln Gln Asp Phe Ile
 245 250 255

ttt tat tca aat gtt gaa gat gac tca acc aat gga ttc cat gat gtc 992
 Phe Tyr Ser Asn Val Glu Asp Asp Ser Thr Asn Gly Phe His Asp Val
 260 265 270 275

tgt gga ccc aac aag gag ctg gat gaa gac acc tgt cag tgt gtc tgc 1040
 Cys Gly Pro Asn Lys Glu Leu Asp Glu Asp Thr Cys Gln Cys Val Cys
 280 285 290

aag ggg ggg ctt cgg cca tct agt tgt gga ccc cac aaa gaa cta gat 1088
 Lys Gly Gly Leu Arg Pro Ser Ser Cys Gly Pro His Lys Glu Leu Asp
 295 300 305

aga gac tca tgt cag tgt gtc tgt aaa aac aaa ctt ttc cct aat tca 1136
 Arg Asp Ser Cys Gln Cys Val Cys Lys Asn Lys Leu Phe Pro Asn Ser
 310 315 320

tgt gga gcc aac agg gaa ttt gat gag aat aca tgt cag tgt gta tgt 1184
 Cys Gly Ala Asn Arg Glu Phe Asp Glu Asn Thr Cys Gln Cys Val Cys
 325 330 335

aaa aga acg tgt cca aga aat cag ccc ctg aat cct ggg aaa tgt gcc 1232
 Lys Arg Thr Cys Pro Arg Asn Gln Pro Leu Asn Pro Gly Lys Cys Ala
 340 345 350 355

tgt gaa tgt aca gaa aac aca cag aag tgc ttc ctt aaa ggg aag aag 1280
 Cys Glu Cys Thr Glu Asn Thr Gln Lys Cys Phe Leu Lys Gly Lys Lys
 360 365 370

ttc cac cat caa aca tgc agt tgt tac aga aga ccg tgt gcg aat cga 1328
 Phe His His Gln Thr Cys Ser Cys Tyr Arg Arg Pro Cys Ala Asn Arg
 375 380 385

ctg aag cat tgt gat cca gga ctg tcc ttt agt gaa gaa gta tgc cgc 1376
 Leu Lys His Cys Asp Pro Gly Leu Ser Phe Ser Glu Glu Val Cys Arg
 390 395 400

tgt gtc cca tgc tat tgg aaa agg cca cat ctg aac taagatcata 1422
 Cys Val Pro Ser Tyr Trp Lys Arg Pro His Leu Asn
 405 410 415

ccagtttttca gtcagtcaca gtcatttact ctcttgaaga ctgttggaac agcacttagc 1482

actgtctatg cacagaaaga ctctgtggga ccacatggta acagaggccc aagtctgtgt 1542

ttattgaacc atgtggatta ctgcgggaga ggactggcac tcatgtgcaa aaaaaacctc 1602

ttcaaagact gggtttctgc cagggaccag acagctgagg tttttctctt gtgatttaaa 1662

aaaagaatga ctatataatt tattttccact aaaaatattg ttcctgcatt catttttata 1722
gcaataacaa ttggtaaagc tcactgtgat cagtattttt ataacatgca aaactatggt 1782
taaaataaaa tgaaaattgt attataaaaa aaaaaaaaaa aaaaaaaaaa gctt 1836

<210> 11
<211> 415
<212> PRT
<213> Murine

<400> 11
Met His Leu Leu Cys Phe Leu Ser Leu Ala Cys Ser Leu Leu Ala Ala
1 5 10 15
Ala Leu Ile Pro Ser Pro Arg Glu Ala Pro Ala Thr Val Ala Ala Phe
20 25 30
Glu Ser Gly Leu Gly Phe Ser Glu Ala Glu Pro Asp Gly Gly Glu Val
35 40 45
Lys Ala Phe Glu Gly Lys Asp Leu Glu Glu Gln Leu Arg Ser Val Ser
50 55 60
Ser Val Asp Glu Leu Met Ser Val Leu Tyr Pro Asp Tyr Trp Lys Met
65 70 75 80
Tyr Lys Cys Gln Leu Arg Lys Gly Gly Trp Gln Gln Pro Thr Leu Asn
85 90 95
Thr Arg Thr Gly Asp Ser Val Lys Phe Ala Ala Ala His Tyr Asn Thr
100 105 110
Glu Ile Leu Lys Ser Ile Asp Asn Glu Trp Arg Lys Thr Gln Cys Met
115 120 125
Pro Arg Glu Val Cys Ile Asp Val Gly Lys Glu Phe Gly Ala Ala Thr
130 135 140
Asn Thr Phe Phe Lys Pro Pro Cys Val Ser Val Tyr Arg Cys Gly Gly
145 150 155 160
Cys Cys Asn Ser Glu Gly Leu Gln Cys Met Asn Thr Ser Thr Gly Tyr
165 170 175
Leu Ser Lys Thr Leu Phe Glu Ile Thr Val Pro Leu Ser Gln Gly Pro
180 185 190
Lys Pro Val Thr Ile Ser Phe Ala Asn His Thr Ser Cys Arg Cys Met
195 200 205
Ser Lys Leu Asp Val Tyr Arg Gln Val His Ser Ile Ile Arg Arg Ser
210 215 220
Leu Pro Ala Thr Leu Pro Gln Cys Gln Ala Ala Asn Lys Thr Cys Pro
225 230 235 240
Thr Asn Tyr Val Trp Asn Asn Tyr Met Cys Arg Cys Leu Ala Gln Gln
245 250 255
Asp Phe Ile Phe Tyr Ser Asn Val Glu Asp Asp Ser Thr Asn Gly Phe
260 265 270

His Asp Val Cys Gly Pro Asn Lys Glu Leu Asp Glu Asp Thr Cys Gln
 275 280 285
 Cys Val Cys Lys Gly Gly Leu Arg Pro Ser Ser Cys Gly Pro His Lys
 290 295 300
 Glu Leu Asp Arg Asp Ser Cys Gln Cys Val Cys Lys Asn Lys Leu Phe
 305 310 315 320
 Pro Asn Ser Cys Gly Ala Asn Arg Glu Phe Asp Glu Asn Thr Cys Gln
 325 330 335
 Cys Val Cys Lys Arg Thr Cys Pro Arg Asn Gln Pro Leu Asn Pro Gly
 340 345 350
 Lys Cys Ala Cys Glu Cys Thr Glu Asn Thr Gln Lys Cys Phe Leu Lys
 355 360 365
 Gly Lys Lys Phe His His Gln Thr Cys Ser Cys Tyr Arg Arg Pro Cys
 370 375 380
 Ala Asn Arg Leu Lys His Cys Asp Pro Gly Leu Ser Phe Ser Glu Glu
 385 390 395 400
 Val Cys Arg Cys Val Pro Ser Tyr Trp Lys Arg Pro His Leu Asn
 405 410 415

<210> 12
 <211> 1/41
 <212> DNA
 <213> Quail

<220>
 <221> CDS
 <222> (453)..(1706)

<220>
 <223> Quail VEGF-C cDNA

<400> 12
 gcccccgcgc agcgcctcgc gcgcagccgc cggggccgggc cggccccgcg agggcgcgct 60
 gcgagcgccc actgggtcct gcttccctcc ttctctccc tctctcct cctccttctc 120
 tctgcgcttt ccacgcctcc cgagcgagcg cacgcctcgga tgtccggttt cctgggtgggt 180
 tttttacctg gcaaagtcgc gataacttcg gtgagaattt gcaaagaggc tgggagctcc 240
 cctgcaggcg tctgggagct gctgccgcgc tcgcatcttc tccatcccgc ggattttact 300
 gccttgata ttgcgagggg agggaggggg gtgaggacag caaaaagaaa ggggtggggg 360
 gggggagaga aaaggaaaag aaggagcctc ggaattgtgc cgcattcct gcgctgcccc 420
 gcgaccccc tccgctctgc catctccgca ca atg cac ttg ctg gag atg ctc 473
 Met His Leu Leu Glu Met Leu
 1 5
 tcc ctg ggc tgc tgc ctc gct gct ggc gcc gtg ctc ctg gga ccc cgg 521
 Ser Leu Gly Cys Cys Leu Ala Ala Gly Ala Val Leu Leu Gly Pro Arg
 10 15 20

cag ccg ccc gtc gcc gcc gcc tac gag tcc ggg cac ggc tac tac gag 569
 Gln Pro Pro Val Ala Ala Tyr Glu Ser Gly His Gly Tyr Tyr Glu
 25 30 35

gag gag ccc ggt gcc ggg gaa ccc aag gct cat gca agc aaa gac ctg 617
 Glu Glu Pro Gly Ala Gly Glu Pro Lys Ala His Ala Ser Lys Asp Leu
 40 45 50 55

gaa gag cag ttg cga tct gtg tcc agt gtg gat gaa ctc atg aca gta 665
 Glu Glu Gln Leu Arg Ser Val Ser Ser Val Asp Glu Leu Met Thr Val
 60 65 70

ctt tac cca gaa tac tgg aaa atg ttc aaa tgt cag ttg agg aaa gga 713
 Leu Tyr Pro Glu Tyr Trp Lys Met Phe Lys Cys Gln Leu Arg Lys Gly
 75 80 85

ggt tgg caa cac aac agg gaa cac tcc agc tct gat aca aga tca gat 761
 Gly Trp Gln His Asn Arg Glu His Ser Ser Ser Asp Thr Arg Ser Asp
 90 95 100

gat tca ttg aaa ttt gcc gca gca cat tat aat gca gag atc ctg aaa 809
 Asp Ser Leu Lys Phe Ala Ala Ala His Tyr Asn Ala Glu Ile Leu Lys
 105 110 115

agt att gat act gaa tgg aga aaa acc cag ggc atg cca cgt gaa gtg 857
 Ser Ile Asp Thr Glu Trp Arg Lys Thr Gln Gly Met Pro Arg Glu Val
 120 125 130 135

tgt gtg gat ttg ggg aaa gag ttt gga gca act aca aac acc ttc ttt 905
 Cys Val Asp Leu Gly Lys Glu Phe Gly Ala Thr Thr Asn Thr Phe Phe
 140 145 150

aaa ccc ccg tgt gta tcc atc tac aga tgt gga ggt tgc tgc aat agt 953
 Lys Pro Pro Cys Val Ser Ile Tyr Arg Cys Gly Gly Cys Cys Asn Ser
 155 160 165

gaa gga ctc cag tgt atg aat atc agc aca aat tac atc agc aag aca 1001
 Glu Gly Leu Gln Cys Met Asn Ile Ser Thr Asn Tyr Ile Ser Lys Thr
 170 175 180

ttg ttt gag att aca gtg cct ctc tct cat ggc ccc aaa cct gta aca 1049
 Leu Phe Glu Ile Thr Val Pro Leu Ser His Gly Pro Lys Pro Val Thr
 185 190 195

gtc agt ttt gcc aat cac acg tcc tgc cga tgc atg tct aag ttg gat 1097
 Val Ser Phe Ala Asn His Thr Ser Cys Arg Cys Met Ser Lys Leu Asp
 200 205 210 215

gtt tac aga caa gtt cat tct atc ata aga cgt tcc ttg cca gca aca 1145
 Val Tyr Arg Gln Val His Ser Ile Ile Arg Arg Ser Leu Pro Ala Thr
 220 225 230

caa act cag tgt cat gtg gca aac aag acc tgt cca aaa aat cat gtc 1193
 Gln Thr Gln Cys His Val Ala Asn Lys Thr Cys Pro Lys Asn His Val
 235 240 245

tgg aat aat cag att tgc aga tgc tta gca cag cac gat ttt ggt ttc 1241
 Trp Asn Asn Gln Ile Cys Arg Cys Leu Ala Gln His Asp Phe Gly Phe
 250 255 260

tct tct cac ctt gga gat tct gac aca tct gaa gga ttc cat att tgt 1289
 Ser Ser His Leu Gly Asp Ser Asp Thr Ser Glu Gly Phe His Ile Cys
 265 270 275

ggg ccc aac aaa gag ctg gat gaa gaa acc tgt caa tgc gtc tgc aaa 1337
 Gly Pro Asn Lys Glu Leu Asp Glu Glu Thr Cys Gln Cys Val Cys Lys
 280 285 290 295
 gga ggt gtg cgg ccc ata agc tgt ggc cct cac aaa gaa cta gac agg 1385
 Gly Gly Val Arg Pro Ile Ser Cys Gly Pro His Lys Glu Leu Asp Arg
 300 305 310
 gca tca tgt cag tgc atg tgc aaa aac aaa ctg ctc ccc agt tcc tgt 1433
 Ala Ser Cys Gln Cys Met Cys Lys Asn Lys Leu Leu Pro Ser Ser Cys
 315 320 325
 ggg cct aac aaa gaa ttt gat gaa gaa aag tgc cag tgt gta tgt aaa 1481
 Gly Pro Asn Lys Glu Phe Asp Glu Glu Lys Cys Gln Cys Val Cys Lys
 330 335 340
 aag acc tgt ccc aaa cat cat cca cta aat cct gca aaa tgc atc tgc 1529
 Lys Thr Cys Pro Lys His His Pro Leu Asn Pro Ala Lys Cys Ile Cys
 345 350 355
 gaa tgt aca gaa tct ccc aat aaa tgt ttc tta aaa gga aaa aga ttt 1577
 Glu Cys Thr Glu Ser Pro Asn Lys Cys Phe Leu Lys Gly Lys Arg Phe
 360 365 370 375
 cat cac cag aca tgc agt tgt tac aga cca cca tgt aca gtc cga acg 1625
 His His Gln Thr Cys Ser Cys Tyr Arg Pro Pro Cys Thr Val Arg Thr
 380 385 390
 aaa cgc tgt gat gct gga ttt ctg tta gct gaa gaa gtg tgc cgc tgt 1673
 Lys Arg Cys Asp Ala Gly Phe Leu Leu Ala Glu Glu Val Cys Arg Cys
 395 400 405
 gta cgc aca tct tgg aaa aga cca ctt atg aat taagcgaaga aagcactact 1726
 Val Arg Thr Ser Trp Lys Arg Pro Leu Met Asn
 410 415
 cgctatatag tgcgc 1741

<210> 13
 <211> 418
 <212> PRT
 <213> Quail

<400> 13
 Met His Leu Leu Glu Met Leu Ser Leu Gly Cys Cys Leu Ala Ala Gly
 1 5 10 15
 Ala Val Leu Leu Gly Pro Arg Gln Pro Pro Val Ala Ala Ala Tyr Glu
 20 25 30
 Ser Gly His Gly Tyr Tyr Glu Glu Glu Pro Gly Ala Gly Glu Pro Lys
 35 40 45
 Ala His Ala Ser Lys Asp Leu Glu Glu Gln Leu Arg Ser Val Ser Ser
 50 55 60
 Val Asp Glu Leu Met Thr Val Leu Tyr Pro Glu Tyr Trp Lys Met Phe
 65 70 75 80
 Lys Cys Gln Leu Arg Lys Gly Gly Trp Gln His Asn Arg Glu His Ser
 85 90 95

Ser Ser Asp Thr Arg Ser Asp Asp Ser Leu Lys Phe Ala Ala Ala His
 100 105 110
 Tyr Asn Ala Glu Ile Leu Lys Ser Ile Asp Thr Glu Trp Arg Lys Thr
 115 120 125
 Gln Gly Met Pro Arg Glu Val Cys Val Asp Leu Gly Lys Glu Phe Gly
 130 135 140
 Ala Thr Thr Asn Thr Phe Phe Lys Pro Pro Cys Val Ser Ile Tyr Arg
 145 150 155 160
 Cys Gly Gly Cys Cys Asn Ser Glu Gly Leu Gln Cys Met Asn Ile Ser
 165 170 175
 Thr Asn Tyr Ile Ser Lys Thr Leu Phe Glu Ile Thr Val Pro Leu Ser
 180 185 190
 His Gly Pro Lys Pro Val Thr Val Ser Phe Ala Asn His Thr Ser Cys
 195 200 205
 Arg Cys Met Ser Lys Leu Asp Val Tyr Arg Gln Val His Ser Ile Ile
 210 215 220
 Arg Arg Ser Leu Pro Ala Thr Gln Thr Gln Cys His Val Ala Asn Lys
 225 230 235 240
 Thr Cys Pro Lys Asn His Val Trp Asn Asn Gln Ile Cys Arg Cys Leu
 245 250 255
 Ala Gln His Asp Phe Gly Phe Ser Ser His Leu Gly Asp Ser Asp Thr
 260 265 270
 Ser Glu Gly Phe His Ile Cys Gly Pro Asn Lys Glu Leu Asp Glu Glu
 275 280 285
 Thr Cys Gln Cys Val Cys Lys Gly Gly Val Arg Pro Ile Ser Cys Gly
 290 295 300
 Pro His Lys Glu Leu Asp Arg Ala Ser Cys Gln Cys Met Cys Lys Asn
 305 310 315 320
 Lys Leu Leu Pro Ser Ser Cys Gly Pro Asn Lys Glu Phe Asp Glu Glu
 325 330 335
 Lys Cys Gln Cys Val Cys Lys Lys Thr Cys Pro Lys His His Pro Leu
 340 345 350
 Asn Pro Ala Lys Cys Ile Cys Glu Cys Thr Glu Ser Pro Asn Lys Cys
 355 360 365
 Phe Leu Lys Gly Lys Arg Phe His His Gln Thr Cys Ser Cys Tyr Arg
 370 375 380
 Pro Pro Cys Thr Val Arg Thr Lys Arg Cys Asp Ala Gly Phe Leu Leu
 385 390 395 400
 Ala Glu Glu Val Cys Arg Cys Val Arg Thr Ser Trp Lys Arg Pro Leu
 405 410 415
 Met Asn

<210> 14
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: peptide

<229>
<223> IgG-Kappa sequence

<400> 14
Ala Val Val Met Thr Gln Thr Pro Ala Ser
1 5 10

<210> 15
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 15
tctcttctgt gcttgagttg ag

22

<210> 16
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 16
tctcttctgt ccttgagttg ag

22

<210> 17
<211> 65
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 17
tgtgtgcag caaattttat agtctcttct gtggcgggcg cgggcgggcg cgcctcgca 60
ggacc 65

<210> 18
<211> 30
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
oligonucleotide

<400> 18 30
ctggcaggga actgctaata atggaatgaa

<210> 19
<211> 84
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 19
gggtccggcg tccgagaggt cgagtcggga ctctgatgg tgatggatgat gggcggcggc 60
ggcggcgggc gctcggcgag gacc 84

<210> 20
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 20 31
gtattataat gtctccacc aaattttata g

<210> 21
<211> 93
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 21 93
gttcgctgcc tgacactgtg gtagtggtgc tggcggccgc tagtgatggg gatggatgatg 60
ataatggaa tgaacttgtc tgtaaacatc cag

<210> 22
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 22 17
catgtacgaa ccgccag

<210> 23

<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 20
aatgacacaga gagaggcgag 20

<210> 24
<211> 24
<212> DNA
<213> Homo sapiens

<400> 24
ggcgaggcca cggtaggtct gcgt 24

<210> 25
<211> 24
<212> DNA
<213> Homo sapiens

<400> 25
tttctttgac aggcttatgc aagc 24

<210> 26
<211> 24
<212> DNA
<213> Homo sapiens

<400> 26
gagatcttga aaagtaagta tggg 24

<210> 27
<211> 23
<212> DNA
<213> Homo sapiens

<400> 27
atgacttgac aggtattgat aat 23

<210> 28
<211> 23
<212> DNA
<213> Homo sapiens

<400> 28
ctcagcaaga cggtgggtat tgt 23

<210> 29
<211> 25
<212> DNA
<213> Homo sapiens

<400> 29
ccctttctttg tagttatttg aaatt 25

<210> 30
<211> 17
<212> DNA
<213> Homo sapiens

<400> 30
aactatccac agtgagtatg aattaaa

27

<210> 31
<211> 24
<212> DNA
<213> Homo sapiens

<400> 31
ttctttcctaaa ggtgtcaggc agcg

24

<210> 32
<211> 21
<212> DNA
<213> Homo sapiens

<400> 32
gctggagatg gtagcagaat g

21

<210> 33
<211> 23
<212> DNA
<213> Homo sapiens

<400> 33
ctatttgtct agactcaaca gat

23

<210> 34
<211> 22
<212> DNA
<213> Homo sapiens

<400> 34
caaacatgca ggtaagagat cc

22

<210> 35
<211> 24
<212> DNA
<213> Homo sapiens

<400> 35
tgttttctcta gctgttacag acgg

24

<210> 36
<211> 24
<212> DNA
<213> Murine

<400> 36
ggcaggtca aggtaggtgc aagg

24

<210> 37
<211> 26
<212> DNA
<213> Murine

<400> 37
attgtctttg acaggctttt tgaagg

26

<210> 38
<211> 21
<212> DNA
<213> Murine

<400> 38
gaatcttga aaagtaagta g

21

<210> 39
<211> 24
<212> DNA
<213> Murine

<400> 39
tgtgactga caggtattga taat

24

<210> 40
<211> 20
<212> DNA
<213> Murine

<400> 40
ctcaggaaga cggtaggtat

20

<210> 41
<211> 25
<212> DNA
<213> Murine

<400> 41
ttgtccttg tagttgtttg aaatt

25

<210> 42
<211> 20
<212> DNA
<213> Murine

<400> 42
acattaccac agtgagtatg

20

<210> 43
<211> 26
<212> DNA
<213> Murine

<400> 43
gtctcccaaa aaggtgtcag gcagct

26

<210> 44
 <211> 23
 <212> DNA
 <213> Murine

<400> 44
 aatgttgaag atggtaagta aaa

23

<210> 45
 <211> 16
 <212> DNA
 <213> Murine

<400> 45
 tetagactca accaat

16

<210> 46
 <211> 22
 <212> DNA
 <213> Murine

<400> 46
 caaacatgca ggtaaggagt gt

22

<210> 47
 <211> 24
 <212> DNA
 <213> Murine

<400> 47
 ttttcacctta gttggttacag aaga

24

<210> 48
 <211> 2991
 <212> DNA
 <213> Homo sapiens

<220>
 <223> Genomic DNA - Sequence upstream of VEGF-C coding
 sequence

<400> 48
 gtttttaagta gagacgggggt ttcaccaacg gttgaaaata tttatcatgg tctccctaag 60
 atggaacgggtg ttagctagga tgggtctcgat ctctgacct catgatccac ccgcctcggc 120
 ctctcaaaagt gctgggatta caggcgtgag ccaccgtgtc cgaccaacct taagacaaac 180
 aactactgca tgattgtttt tggagacctt ttttttatte aaataaattt ttgccagcat 240
 tttctgactc aaagtatagc agcaggaaga taacactttt gtgagaaaaa agtttgaata 300
 cagcttactg ctgtatttaa atgaaacagt agttaatatg atattaatat attttggata 360
 tattttgagt ttgttgattt tccagtcttc acccgtgtgt aggctgtgtg gtgttggaaa 420
 tgcctgtgtt tctcaatttt gtttgccat tagaatctg atgtccaagc cttactccag 480
 ttagaccagt taagccagaa aggcagaagg tgtactcaag catctgtttt ttcaaaatct 540

cctttttgtga tgcdaagtgc aatcaaaagtt tagaatcatt gtaataagcaa atgggttgaat 600
 ggaaaactcca cctttctatcc aaatccctacc ccagttctgcc ctttagctgtt ctctttttcac 660
 agatctatca atgtctgaag ataactatgg caggtctgac aaatatgcac agagcaggaa 720
 gacagcaaga gagtcataca ctgaccatgt tccaaatcac aaaacatctc aacaggctag 780
 atcatggacc gagtctgatg ggatggaatt tcataaagat acataaaaaa gcctcttgga 840
 tacagtaaac ttaactccac aaatacaggg gaatttagac gtgactaagt agcagtcacat 900
 atgaaaaatt attgaggaat ttgtttgact ttaagggtag tgtgagtcaa cactgtgatt 960
 tggctgccag aaaataaact caatccaagg ctgtatcaac aaaggcatac tgtccattct 1020
 gcctgctcat tacagcacta agtaccgagc catgtttctc accgcatact tcatgaacat 1080
 ggaaagctaa cagtatgggt aaggggggaa actggaactg tcatcttggg gaataaaagg 1140
 gatatttagc caggagtaaa gttagcttag ggagaccatg ataaatattt tcaaaatatt 1200
 tgaaggactc agttgtggaa gtgagattag atttattgtg taaaactcca ggagtcaaaa 1260
 gcaatagaga gatagaagga aatgcttttc agcagtgttg ctcatcaata aaggagtgta 1320
 acagccacac agaattggaag gttccctgtc ctttgagata tttaagcctt caagtaaat 1380
 atgggtgagg agtttcaaat cttaggttga accagataag aaagtctctt ctcccggtaa 1440
 gatattatgg acctataaca tctgtgtact taaaagtaga ttgggagtga aaggcagact 1500
 tttgatgttc tgtacactgt tgaaacctt tagcgtggtc ctctgtaacc tgcctacct 1560
 gccccaaagg ggcagctagc caatgccacc agcccaacgg aaaccccagt gcttttccaa 1620
 tggggaaatg cagtcacttt tctttggatg ctacacatcc tttctggaat atgtctcaca 1680
 cacatctctc tttatcacc cctttttcaa gtaaaccaac ttcttgaga agctgacaat 1740
 gtgtctcttt actctccacg aagattctgg cctttctctt cactgtcag aagtttagga 1800
 ttccaaaggg atcattagca tccatcccaa cagcctgcac tgcctctga gaactgcgg 1860
 tcttgatca tcaggcaact ttcaactaca cagaccaagg gagagagggg accctccga 1920
 ggtcccatag ggttctctga catagtgatg acctttttcc aaactttgag cagggcgctg 1980
 ggggcagggc gtgcgggagg gaggacaaga actcgggagt ggcagaggat aaagcggggg 2040
 ctccctccac cccacgggtc ccagtttctc cccgtgcac gtggtccagg gtggtcgcac 2100
 cactctaaa gccgggtccc ccaaccgcca gccccgggac tgaacttgcc cctccggccg 2160
 cccgtctccc gcaggggaca ggggcgggga gggagagatc cagagggggg ctgggggagg 2220
 tggggccgcc ggggaggagg cgagggaac ggggagctcc agggagacgg ctccgaggg 2280
 agagtgagag gggagggcag cccgggctcg gcacgtccc tccctcgcc gctttctctc 2340
 acataagcgc aggcagaggg ccgtcagtc atgcctgcc cctgcgcccg ccgccgccgc 2400
 cgccgccgt cagccggcg ccgtctggag gactctgcgc cggggcgctc cggggcccg 2460

ccgagggcag cggccccggc ggccctctct cggccccggg caccggcggc agcggccccg 2520
 ccgagggccc cggggccccg ctctctctac ttcggggaag gggagggagg agggggacga 2580
 ggggtcttgg gggtttggag gggtgaaca tcggggggtg ttctggtgtc cccgccccg 2640
 ctctctcaaa aagctacacc gacggggacc ggggggggt cctccctcgc cctcgcttca 2700
 cctcgggggc tcgaatgag gggagctcgg atgtccggtt tctgtgagg cttttacctg 2760
 aatccggcgg cctttccccg gcactggctg ggagggcgcc ctgcaaagtt gggaacgcgg 2820
 agcccgaggc ccgtcccgcc cgcctccggc tcgccaggg ggggtcgccg ggaggagccc 2880
 gggggagagg gaccaggagg gggccggcgc ctgcagggg cggccgcgcc cccacccctg 2940
 ccccgccag cggaccggtc cccaccccc ggtccttcca ccatgcactt g 2991

<210> 49
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:
 oligonucleotide

400 49 20
 cagggttat gcaagcaaag

210 50
 211 20
 212 DNA
 213 Artificial Sequence

220
 223 Description of Artificial Sequence:
 oligonucleotide

400 50 20
 aacacagttt tcataatag

210 51
 211 19
 212 PRT
 213 Homo sapiens

400 51
 Leu Ser Lys Thr Val Ser Gly Ser Glu Gln Asp Leu Pro His Glu Leu
 1 5 10 15

His Val Glu

210 52
 211 25
 212 DNA
 213 Artificial Sequence

<220>
 <223> Description of Artificial Sequence:
 oligonucleotide

<400> 52
 gatggacaca gatggaggtt taaag

25

<210> 53
 <211> 196
 <212> PRT
 <213> Homo sapiens

<220>
 <223> Human PDGF-A

<400> 53
 Met Arg Thr Leu Ala Cys Leu Leu Leu Leu Gly Cys Gly Tyr Leu Ala
 1 5 10 15
 His Val Leu Ala Glu Glu Ala Glu Ile Pro Arg Glu Val Ile Glu Arg
 20 25 30
 Leu Ala Arg Ser Gln Ile His Ser Ile Arg Asp Leu Gln Arg Leu Leu
 35 40 45
 Glu Ile Asp Ser Val Gly Ser Glu Asp Ser Leu Asp Thr Ser Leu Arg
 50 55 60
 Ala His Gly Val His Ala Thr Lys His Val Pro Glu Lys Arg Pro Leu
 65 70 75 80
 Pro Ile Arg Arg Lys Arg Ser Ile Glu Glu Ala Val Pro Ala Val Cys
 85 90 95
 Lys Thr Arg Thr Val Ile Tyr Glu Ile Pro Arg Ser Gln Val Asp Pro
 100 105 110
 Thr Ser Ala Asn Phe Leu Ile Trp Pro Pro Cys Val Glu Val Lys Arg
 115 120 125
 Cys Thr Gly Cys Cys Asn Thr Ser Ser Val Lys Cys Gln Pro Ser Arg
 130 135 140
 Val His His Arg Ser Val Lys Val Ala Lys Val Glu Tyr Val Arg Lys
 145 150 155 160
 Lys Pro Lys Leu Lys Glu Val Gln Val Arg Leu Glu Glu His Leu Glu
 165 170 175
 Cys Ala Cys Ala Thr Thr Ser Leu Asn Pro Asp Tyr Arg Glu Glu Asp
 180 185 190
 Thr Asp Val Arg
 195

<210> 54
 <211> 241
 <212> PRT
 <213> Homo sapiens

<220>

<223> Human PDGF B

<400> 54

Met Asn Arg Cys Trp Ala Leu Phe Leu Ser Leu Cys Cys Tyr Leu Arg
1 5 10 15
Leu Val Ser Ala Glu Gly Asp Pro Ile Pro Glu Glu Leu Tyr Glu Met
20 25 30
Leu Ser Asp His Ser Ile Arg Ser Phe Asp Asp Leu Gln Arg Leu Leu
35 40 45
His Gly Asp Pro Gly Glu Glu Asp Gly Ala Glu Leu Asp Leu Asn Met
50 55 60
Thr Arg Ser His Ser Gly Gly Glu Leu Glu Ser Leu Ala Arg Gly Arg
65 70 75 80
Arg Ser Leu Gly Ser Leu Thr Ile Ala Glu Pro Ala Met Ile Ala Glu
85 90 95
Cys Lys Thr Arg Thr Glu Val Phe Glu Ile Ser Arg Arg Leu Ile Asp
100 105 110
Arg Thr Asn Ala Asn Phe Leu Val Trp Pro Pro Cys Val Glu Val Gln
115 120 125
Arg Cys Ser Gly Cys Cys Asn Asn Arg Asn Val Gln Cys Arg Pro Thr
130 135 140
Gln Val Gln Leu Arg Pro Val Gln Val Arg Lys Ile Glu Ile Val Arg
145 150 155 160
Lys Lys Pro Ile Phe Lys Lys Ala Thr Val Thr Leu Glu Asp His Leu
165 170 175
Ala Cys Lys Cys Glu Thr Val Ala Ala Ala Arg Pro Val Thr Arg Ser
180 185 190
Pro Gly Gly Ser Gln Glu Gln Arg Ala Lys Thr Pro Gln Thr Arg Val
195 200 205
Thr Ile Arg Thr Val Arg Val Arg Arg Pro Pro Lys Gly Lys His Arg
210 215 220
Lys Phe Lys His Thr His Asp Lys Thr Ala Leu Lys Glu Thr Leu Gly
225 230 235 240
Ala

<210> 55

<211> 149

<212> PRT

<213> Homo sapiens

<220>

<223> Human PIGF

<400> 55

Met Pro Val Met Arg Leu Phe Pro Cys Phe Leu Gln Leu Leu Ala Gly
 1 5 10 15
 Leu Ala Leu Pro Ala Val Pro Pro Gln Gln Trp Ala Leu Ser Ala Gly
 20 25 30
 Asn Gly Ser Ser Glu Val Glu Val Val Pro Phe Gln Glu Val Trp Gly
 35 40 45
 Arg Ser Tyr Cys Arg Ala Leu Glu Arg Leu Val Asp Val Val Ser Glu
 50 55 60
 Tyr Pro Ser Glu Val Glu His Met Phe Ser Pro Ser Cys Val Ser Leu
 65 70 75 80
 Leu Arg Cys Thr Gly Cys Cys Gly Asp Glu Asn Leu His Cys Val Pro
 85 90 95
 Val Glu Thr Ala Asn Val Thr Met Gln Leu Leu Lys Ile Arg Ser Gly
 100 105 110
 Asp Arg Pro Ser Tyr Val Glu Leu Thr Phe Ser Gln His Val Arg Cys
 115 120 125
 Glu Cys Arg Pro Leu Arg Glu Lys Met Lys Pro Glu Arg Cys Gly Asp
 130 135 140
 Ala Val Pro Arg Arg
 145

<210> 56
 <211> 191
 <212> PRT
 <213> Homo sapiens

<220>
 <223> VEGF165 precursor

<400> 56
 Met Asn Phe Leu Leu Ser Trp Val His Trp Ser Leu Ala Leu Leu Leu
 1 5 10 15
 Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Met Ala Glu Gly
 20 25 30
 Gly Gly Gln Asn His His Glu Val Val Lys Phe Met Asp Val Tyr Gln
 35 40 45
 Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu
 50 55 60
 Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu
 65 70 75 80
 Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu Glu Cys Val Pro
 85 90 95
 Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro His
 100 105 110
 Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln His Asn Lys Cys
 115 120 125

Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu Asn Pro Cys Gly
 130 135 140

Pro Cys Ser Glu Arg Arg Lys His Leu Phe Val Gln Asp Pro Gln Thr
 145 150 155 160

Cys Lys Cys Ser Cys Lys Asn Thr Asp Ser Arg Cys Lys Ala Arg Gln
 165 170 175

Leu Glu Leu Asn Glu Arg Thr Cys Arg Cys Asp Lys Pro Arg Arg
 180 185 190

<210> 57

<211> 188

<212> PRT

<213> Homo sapiens

<220>

<223> VEGF-B167

<400> 57

Met Ser Pro Leu Leu Arg Arg Leu Leu Leu Ala Ala Leu Leu Gln Leu
 1 5 10 15

Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His Gln
 20 25 30

Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys Gln
 35 40 45

Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr Val
 50 55 60

Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly Gly
 65 70 75 80

Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His Gln
 85 90 95

Val Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu Gly
 100 105 110

Glu Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys Lys
 115 120 125

Lys Asp Ser Ala Val Lys Pro Asp Ser Pro Arg Pro Leu Cys Pro Arg
 130 135 140

Cys Thr Gln His His Gln Arg Pro Asp Pro Arg Thr Cys Arg Cys Arg
 145 150 155 160

Cys Arg Arg Arg Ser Phe Leu Arg Cys Gln Gly Arg Gly Leu Glu Leu
 165 170 175

Asn Pro Asp Thr Cys Arg Cys Arg Lys Leu Arg Arg
 180 185

<210> 58

<211> 419

<212> PPT

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: VEGF C delta Cys156 mutant

<220>
<223> At position 156, "Xaa" can be anything other than cysteine or can be nothing

<400> 58
Met His Leu Leu Gly Phe Phe Ser Val Ala Cys Ser Leu Leu Ala Ala
1 5 10 15
Ala Leu Leu Pro Gly Pro Arg Glu Ala Pro Ala Ala Ala Ala Phe
20 25 30
Glu Ser Gly Leu Asp Leu Ser Asp Ala Glu Pro Asp Ala Gly Glu Ala
35 40 45
Thr Ala Tyr Ala Ser Lys Asp Leu Glu Glu Gln Leu Arg Ser Val Ser
50 55 60
Ser Val Asp Glu Leu Met Thr Val Leu Tyr Pro Glu Tyr Trp Lys Met
65 70 75 80
Tyr Lys Cys Gln Leu Arg Lys Gly Gly Trp Gln His Asn Arg Glu Gln
85 90 95
Ala Asn Leu Asn Ser Arg Thr Glu Glu Thr Ile Lys Phe Ala Ala Ala
100 105 110
His Tyr Asn Thr Glu Ile Leu Lys Ser Ile Asp Asn Glu Trp Arg Lys
115 120 125
Thr Gln Cys Met Pro Arg Glu Val Cys Ile Asp Val Gly Lys Glu Phe
130 135 140
Gly Val Ala Thr Asn Thr Phe Phe Lys Pro Pro Xaa Val Ser Val Tyr
145 150 155 160
Arg Cys Gly Gly Cys Cys Asn Ser Glu Gly Leu Gln Cys Met Asn Thr
165 170 175
Ser Thr Ser Tyr Leu Ser Lys Thr Leu Phe Glu Ile Thr Val Pro Leu
180 185 190
Ser Gln Gly Pro Lys Pro Val Thr Ile Ser Phe Ala Asn His Thr Ser
195 200 205
Cys Arg Cys Met Ser Lys Leu Asp Val Tyr Arg Gln Val His Ser Ile
210 215 220
Ile Arg Arg Ser Leu Pro Ala Thr Leu Pro Gln Cys Gln Ala Ala Asn
225 230 235 240
Lys Thr Cys Pro Thr Asn Tyr Met Trp Asn Asn His Ile Cys Arg Cys
245 250 255
Leu Ala Gln Glu Asp Phe Met Phe Ser Ser Asp Ala Gly Asp Asp Ser
260 265 270
Thr Asp Gly Phe His Asp Ile Cys Gly Pro Asn Lys Glu Leu Asp Glu
275 280 285

Glu Thr Cys Gln Cys Val Cys Arg Ala Gly Leu Arg Pro Ala Ser Cys
 290 295 300

Gly Pro His Lys Glu Leu Asp Arg Asn Ser Cys Gln Cys Val Cys Lys
 305 310 315 320

Asn Lys Leu Phe Pro Ser Gln Cys Gly Ala Asn Arg Glu Phe Asp Glu
 325 330 335

Asn Thr Cys Gln Cys Val Cys Lys Arg Thr Cys Pro Arg Asn Gln Pro
 340 345 350

Leu Asn Pro Gly Lys Cys Ala Cys Glu Cys Thr Glu Ser Pro Gln Lys
 355 360 365

Cys Leu Leu Lys Gly Lys Lys Phe His His Gln Thr Cys Ser Cys Tyr
 370 375 380

Arg Arg Pro Cys Thr Asn Arg Gln Lys Ala Cys Glu Pro Gly Phe Ser
 385 390 395 400

Tyr Ser Glu Glu Val Cys Arg Cys Val Pro Ser Tyr Trp Lys Arg Pro
 405 410 415

Gln Met Ser

<210> 59

<211> 160

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: VEGF-C delta N delta CHis

<400> 59

Met His Leu Leu Gly Phe Phe Ser Val Ala Cys Ser Leu Leu Ala Ala
 1 5 10 15

Ala Leu Leu Pro Gly Pro Arg Glu Ala Pro Ala Ala Ala Ala Thr
 20 25 30

Glu Glu Thr Ile Lys Phe Ala Ala Ala His Tyr Asn Thr Glu Ile Leu
 35 40 45

Lys Ser Ile Asp Asn Glu Trp Arg Lys Thr Gln Cys Met Pro Arg Glu
 50 55 60

Val Cys Ile Asp Val Gly Lys Glu Phe Gly Val Ala Thr Asn Thr Phe
 65 70 75 80

Phe Lys Pro Pro Cys Val Ser Val Tyr Arg Cys Gly Gly Cys Cys Asn
 85 90 95

Ser Glu Gly Leu Gln Cys Met Asn Thr Ser Thr Ser Tyr Leu Ser Lys
 100 105 110

Thr Leu Phe Glu Ile Thr Val Pro Leu Ser Gln Gly Pro Lys Pro Val
 115 120 125

Thr Ile Ser Phe Ala Asn His Thr Ser Cys Arg Cys Met Ser Lys Leu
130 135 140

Asp Val Tyr Arg Gln Val His Ser Ile Ile His His His His His His
145 150 155 160